REMARKS

Claims 15-22 and 24-26 are pending in the application. Claims 1-14, 23 and 27-34 are withdrawn from consideration as being drawn to non-elected inventions. Applicants expressly reserve the right to file divisional applications or take such other appropriate measures deemed necessary to protect the inventions in the remaining claims.

Claims 15-22 and 24-26 are being examined to the extent they read on SEQ ID NO: 3. The claims have been amended to remove reference to non-elected sequences. Applicants expressly reserve the right to file divisional applications or take such other appropriate measures deemed necessary to protect the invention as it pertains to the remaining sequences.

Claims 15, 16, 19, 24, 25 and 26 (and thus dependent claims 17, 18, and 20-22) have been amended. Support for the amendments can be found in the specification as filed. No new matter has been added by way of amendment. Reexamination and reconsideration of the claims are respectfully requested.

Sequence Identifiers

In the previous office action of November 27, 2002, the Examiner stated that Figures 4 and 5 were missing sequence identifiers. Applicants submitted proposed drawing changes with their response of December 16, 2002, and advised the Examiner that formal drawings in compliance with 37 CFR §1.84, including those changes, would be filed upon approval of the amendments by the Examiner and upon notification of allowable subject matter. In the instant Office Action, the Examiner requires the amendment of the Brief Description of the Drawings for figures 4 and 5. Applicants have made these required amendments and again assure the Examiner that formal drawings in compliance with 37 CFR §1.84 will be filed upon approval of the amendments by the Examiner and upon notification of allowable subject matter

Abstract

The Examiner has objected to the abstract of the invention as not being descriptive of the instant invention. Applicants have amended the abstract as shown in the previous section entitled "Amendments to the Specification", beginning on page 2 of the instant response. Applicants assert that the new abstract is clearly indicative of the invention to which the claims are directed. No new matter is added by way of the amendment to the abstract.

Title

The Examiner has objected to the title of the invention as not being descriptive of the instant invention. Applicants have amended the title to "SCLEROTINIA-INDUCIBLE LIPID-TRANSFER POLYNUCLEOTIDES AND THEIR USES IN PLANT DISEASE RESISTANCE", in order to more clearly indicate the invention to which the claims are directed. This amendment is shown in the previous section entitled "Amendments to the Specification", beginning on page 2 of the instant response. No new matter is added by way of the amendment to the title.

Hyperlinks

The Examiner has objected to the disclosure due to the inclusion of a hyperlink on page 13, lines 18-19. Applicants have amended the specification to remove the hyperlink, thereby obviating this objection.

Claim Objections

The Examiner has objected to claims 15 and 25 because they contain non-elected sequences. Applicants have amended claims 15 and 25 to remove reference to non-elected sequences. The Examiner has also objected to claim 16 because there is an improper article before "nucleotide" in line 1. Applicants have amended claim 16 to correct the article. In view of these amendments, Applicants respectfully request that the claim objections be withdrawn.

The Rejection of Claims Under 35 U.S.C. §112, First Paragraph, Should be Withdrawn

Enablement

The Examiner has rejected claims 15-22 and 24-26 under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. Applicants respectfully disagree.

The Examiner states that the instant specification fails to provide guidance for lipid transfer protein-encoding nucleic acids with 70% identity to SEQ ID NO: 3, nucleic acids comprising at least 16 contiguous nucleotides of a nucleic acid that encodes SEQ ID NO: 4, or nucleic acids that hybridize to the latter nucleic acids. The Examiner further states that the instant specification fails to provide guidance for exact hybridization or amplification conditions and probes/primers to use in isolation of nucleic acids other than SEQ ID NO: 3. Applicants respectfully disagree.

Applicants have provided extensive guidance to be used in the selection of stringency conditions based on the desired outcome. See page 10, line 4 through page 11, line 26 of the specification as originally filed. Applicants have also provided an extensive discussion of specific exemplary low, medium and high stringency hybridization conditions and requirements on page 10, lines 14-27. The design of appropriate primers has been outlined by the Applicants on page 25, lines 3 to 14. Furthermore, Applicants have given guidance regarding the design and use of probes on page 25, line 15 through page 26, line 11. In view of the extensive guidance provided, Applicants assert that the invention is clearly enabled as claimed. However, in order to further prosecution, Applicants have amended claims 15 and 25 to remove reference to nucleic acids comprising 16 contiguous nucleotides of SEQ ID NO: 3. Applicants have also amended claims 15 and 25 to recite specific high stringency hybridization conditions as provided in the specification as filed, specifically as given on page 10, lines 24 to 27.

The Examiner states: " The specification ... suggests making variant nucleic acids by making conservative substitutions in the encoded protein. However making such 'conservative' substitutions ... does not produce predictable results." In support of this rejection, the Examiner cites Lazar *et al.* who teach that a conservative substitution reduced biological function while

"nonconservative" substitutions had no effect. Likewise, the Examiner cites Hill *et al.* who teach that ADP-glucose pyrophosphorylase proteins mutated to substitute arginine for histidine (a "conservative" substitution), reduced the enzymes activity. The Examiner concludes that "all these mutated proteins however, would have at least 95% identity to the original protein and the nucleic acids encoding all these mutated proteins would hybridize under high stringency to the nucleic acids encoding the original protein."

Present claim 15 and 25 recite: "... a nucleotide sequence having at least 95% identity with SEQ ID NO:3, *wherein said nucleotide sequence encodes a polypeptide having lipid transfer activity* ...." (emphasis added). It is respectfully pointed out that non-operative embodiments are not claimed. Only those variants *having lipid transfer activity* are claimed.

The specification clearly states on page 23, lines 13-16: "Guidance as to appropriate amino acid substitutions that *do not affect desired biological activity* of the native protein may be found in the model of Dayhoff *et al.* (1978) *Atlas of Protein Sequence and Structure* (Nat'l Biomed. Res. Found., Washington, D.C.), herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar properties, may be preferable.." (emphasis added). The disclosure plainly acknowledges that conservative substitutions per se, *may* not produce a *functional* protein, but is one of many tools the skilled artisan may use to produce a nucleic acid of the currently claimed invention.

Applicants wish to point out that both references use the known homology to related proteins to identify and target particular amino acid residues. These references use homology to predict important conserved amino acids where substitution with another amino acid would actually be likely to have an impact on the activity of the protein. For example, Lazar *et al.* shows that even conservative substitution of L48 with similar amino acids (M or I) dramatically impacted activity, as predicted by the observed absolute conservation of leucine (L) at this position. In all cases, the modified protein had to be screened for the effect(s) of the modification. Clearly, one of skill in the art does believe that structural identity, as well as the presence of functional domains and conserved motifs are predictive of polypeptide function, as is clearly demonstrated by the pervasive use of sequence searching algorithms such as BLAST,

FASTA, and the like, and multiple sequence alignment programs such as CLUSTAL and PileUp, and the like. Accordingly, one of skill in the art could use the known homology to related proteins to identify and target particular amino acid residues where substitution with another amino acid would actually be *unlikely* to have an impact on the activity of the protein.

The screening of a group of sequences containing from a few to many, inoperative species in order to isolate one or more operative species is a common practice in many aspects of the biotechnological arts. With the guidance provided in the specification as cited herein and in the previous responses, isolation of operative embodiments from a group of candidate sequences as claimed in present claims 15 or 25, clearly has a reasonable expectation of success by one skilled in the art.

The Examiner states that it is not clear that the instant nucleic acid actually encodes an LTP involved in a defense reaction. The Examiner states that a search of GenBank found no sequence in either the nucleotide or protein databases that matched the GenBank Accession Numbers listed on page 58, lines 4-12 of the specification. Applicants note that in fact, the numbers provided in the specification as filed are SwissProt accession numbers, not GenBank accession numbers. Applicants have amended the specification to indicate that these are in fact SwissProt database accession numbers. Applicants attach printouts of each of these sequences from the SwissProt database in order to show that the sequence numbers and organisms from which the sequences originate were correctly identified in the specification as originally filed. In addition, one sequence was identified by its SwissProt locus identifier (NLTP-VIGUN) rather than its SwissProt accession number, which is Q43681. Two typographical errors also occurred in the SwissProt accession numbers. Both O64431 and O81135 were prefaced with a Q rather than an O. Applicants have amended the specification to correct these errors.

Applicants attach a print-out of each of the cited sequences as Appendix A, as well as a GAP alignment for each sequence compared to SEQ ID NO: 4 showing the % identity and % similarity scores using the GAP algorithm (Appendix B). Applicants also attach a multiple sequence alignment (Appendix C) showing the highly conserved nature of these lipid transfer proteins, particularly in the second half of the sequences. Identical amino acids are shown in yellow

highlighting and highly conserved amino acids are shown in green highlighting. Applicants assert that these alignments clearly indicate the identity of SEQ ID NO: 4 as a lipid transfer protein.

The Examiner has also rejected claims 15-22 and 24-26 because the specification does not disclose a repeatable process to obtain the nucleic acids (of Patent Deposit No. PTA-2182) and it is not apparent if the nucleic acids are really available to the public. Applicants direct the attention of the Examiner to page 20, lines 7-13 of the specification as originally filed, which clearly states that the deposit of the nucleic acids was made at the Patent Depository of the American Type Culture Collection, Manassas, Virginia, on June 30, 2000, and assigned Patent Deposit No. PTA-2182. Furthermore, the specification clearly states that this deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. The undersigned attorney for Applicants hereby states that the deposits will be irrevocably and without restriction released to the public upon the issuance of a patent.

Written Description

The Examiner has rejected claims 15-22 and 24-26 under 35 U.S.C. §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention.

The Examiner states that the Applicants have not, in fact, described lipid transfer protein-encoding nucleic acids with 70% identity to SEQ ID NO: 3, nucleic acids comprising at least 16 contiguous nucleotides of a nucleic acid that encodes SEQ ID NO: 4, or nucleic acids that hybridize to nucleic acids comprising at least 16 contiguous nucleotides of a nucleic acid that encodes SEQ ID NO:4, and the specification fails to provide an adequate written description of the invention. Applicants respectfully disagree. In view of the claim amendments previously discussed, nucleic acids that comprise 16 contiguous nucleotides of SEQ ID NO:3 are no longer being claimed. Furthermore, nucleic acids with 70% identity to SEQ ID NO: 3 are also no longer being claimed.

Applicants have given clear guidance of hybridization conditions and requirements as discussed *supra*. Furthermore, in order to expedite prosecution, Applicants have amended the claims to clearly specify the exact high stringency hybridization conditions required. As such, the written description is clearly adequate and commensurate with the claims.

Accordingly, Applicants request that the rejections of claims 15-22 and 24-26 under 35 U.S.C. §112, first paragraph, be withdrawn.

The Rejection of Claims Under 35 U.S.C. §112, Second Paragraph, Should be Withdrawn

The Examiner has rejected claims 15-22 and 24-26 under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention.

Applicants have amended claims 15 and 25 to remove part (d).

Applicants have also amended claims 15 and 25 to specifically recite highly stringent conditions, supported by the specification as originally filed on page 10, line 4 through page 11, line 26, more specifically on page 10, lines 24 to 27.

Applicants have amended claims 16, 19 and 24 to correct antecedent basis.

Applicants have amended claim 26 as suggested by the Examiner to clarify that the seed comprises the DNA construct of claim 25.

Accordingly, Applicants respectfully request withdrawal of the rejections of claims 15-22 and 24-26 under 35 U.S.C. §112, second paragraph.

The Rejection of Claims Under 35 U.S.C. §102 Should be Withdrawn

The Examiner has rejected claims 15-21 and 24-26 under 35 U.S.C. 102(b) as being anticipated by Kragh *et al.* (WO 95/11306). Kragh *et al.* teach isolated nucleic acids comprising 21 contiguous nucleotides of a nucleic acid that encodes SEQ ID NO:4. In view of the claim amendments removing reference to isolated nucleic acids comprising at least 16 contiguous nucleotide segments of SEQ ID NO: 3, Applicants assert that the Kragh *et al.* reference no longer applies as 35 U.S.C. 102(b) art.

The Examiner has rejected claim 15 under 35 U.S.C. 102(a) as being anticipated by Or *et al.* (2000, GenBank Accession No. AF195867), based on the Examiner's suggestion that the nucleic acid sequence taught by Or *et al.* would hybridize to SEQ ID NO: 3 under "stringent conditions." Applicants respectfully disagree. Applicants present a GAP alignment of AF195867 compared to SEQ ID NO: 3, showing that the percent identity between these two sequences is 46%. Applicants assert that under the highly stringent conditions recited in amended claim 15, AF195867 would not hybridize to SEQ ID NO: 3 due to its relatively low homology. Accordingly, Applicants assert that claim 15 is not anticipated by the nucleic acid sequence taught by Or *et al.*

The Examiner has rejected claims 15-20, 22 and 24-26 under 35 U.S.C. 102 (b) as being anticipated by Dixon *et al.* (WO 98/51801) because Dixon *et al.* teach an isolated nucleic acid that would hybridize under "stringent conditions" to SEQ ID NO: 3 or nucleic acids that comprise at least 16 contiguous nucleotides of a nucleic acid encoding SEQ ID NO: 4. Applicants present a GAP alignment of SEQ ID NO: 1 from Dixon *et al.* compared to SEQ ID NO: 3, showing that the percent identity between these two sequences is 40.6%. Applicants also note that there are no identical regions of 16 contiguous nucleotides or more between the two sequences. Applicants assert that under the highly stringent conditions recited in amended claims 15 and 25, SEQ ID NO: 1 from Dixon *et al.* would not hybridize to SEQ ID NO: 3 due to its relatively low homology. Accordingly, Applicants assert that claims 15-20, 22 and 24-26 are not anticipated by the nucleic acid sequence taught by Dixon *et al.*

In view of the preceding remarks and claim amendments, Applicants respectfully request withdrawal of the rejections of the claims under 35 U.S.C. §102.

CONCLUSION

In view of the above amendments and remarks, Applicants submit that the rejections of the claims under 35 U.S.C. §§112, first and second paragraphs and 35 U.S.C § 102(a) and (b) have been overcome. Applicants respectfully submit that this application is now in condition for allowance. Early notice to this effect is solicited.

If in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject Application, the Examiner is invited to call the undersigned.

It is not believed that extensions of time or fees for net addition of claims are required, beyond those that may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR §1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-1852.

Respectfully submitted,

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Appendix A

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ID   O81135      PRELIMINARY;      PRT;    92 AA.
AC   O81135;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   7 kDa lipid transfer protein.
GN   LTP-NE.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Morex; TISSUE=Nucellar outer cell layer;
RA   Chen F., Foolad M.R.;
RT   "Nucellar cell-specific expression of a lipid transfer protein gene in
RT   barley.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF039024; AAC28263.1; -.
DR   InterPro; IPR003612; AAI.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
SQ   SEQUENCE   92 AA;  9571 MW;  B6A3F562FF6EC2D9 CRC64;
     MAMRKTKELL LVAMMLALVV AARAAPCEVG QLTVCMPAIT TGAKPSGACC ANLGAQQGCF
     CQYAKDPALG RYITSPHARD TLLSCGLAVP RC
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ID   Q40631      PRELIMINARY;      PRT;    96 AA.
AC   Q40631;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 22, Last annotation update)
DE   Lipid transfer protein.
GN   LTP-2.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IR36;
RX   MEDLINE=98316705; PubMed=9654133;
RA   Garcia-Garrido J.M., Menossi M., Puigdomenech P.,
RA   Martinez-Izquierdo J.A., Delseny M.;
RT   "Characterization of a gene encoding an abscisic acid-inducible type-2
RT   lipid transfer protein from rice.";
RL   FEBS Lett. 428:193-199(1998).
DR   EMBL; U16721; AAC50030.1; -.
DR   Gramene; Q40631; -.
DR   InterPro; IPR003612; AAI.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
SQ   SEQUENCE   96 AA;  9606 MW;  1FFEFC4DEDE337B1 CRC64;
     MMRKLAVLVL AVAMVAACGG GVVGVAGASC NAGQLTVCAA AIAGGARPTA ACCSSLRAQQ
     GCFCQFAKDP RYGRYVNNPN ARKTVSSCGI ALPTCH
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ID   O64431      PRELIMINARY;      PRT;    86 AA.
AC   O64431;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Lipid transfer protein (Fragment).
GN   PEC-1.
OS   Brassica campestris (Field mustard).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Brassica.
OX   NCBI_TaxID=3711;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Anther;
RX   MEDLINE=98198560; PubMed=9539157;
RA   Toriyama K., Hanaoka K., Okada T., Watanabe M.;
RT   "Molecular cloning of a cDNA encoding a pollen extracellular protein
RT   as a potential source of a pollen allergen in Brassica rapa.";
RL   FEBS Lett. 424:234-238(1998).
DR   EMBL; AB010436; BAA25680.1; -.
DR   InterPro; IPR003612; AAI.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   86 AA;  8944 MW;  9240AC49F97D9117 CRC64;
     ILLTLFPAPN EAADTNVEAA CDPKQLQPCL AAITGGGQPS GDCCAKLKEQ QPCLCGFSKN
     PAFAQYISSP NSRKVLTACG IPYPSC
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ID   Q42392      PRELIMINARY;      PRT;    95 AA.
AC   Q42392;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Putative nonspecific lipid transfer protein.
OS   Zinnia elegans.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
OC   Heliantheae; Zinnia.
OX   NCBI_TaxID=34245;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PETER PAN;
RX   MEDLINE=94094560; PubMed=8022936;
RA   Ye Z.H., Varner J.E.;
RT   "Gene expression patterns associated with in vitro tracheary element
RT   formation in isolated single mesophyll cells of Zinnia elegans.";
RL   Plant Physiol. 103:805-813(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PETER PAN;
RA   Ye Z.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Xylem;
RX   MEDLINE=94094561; PubMed=8022937;
RA   Demura T., Fukuda H.;
RT   "Molecular cloning and characterization of cDNAs associated with
RT   tracheary element differentiation in cultured Zinnia cells.";
RL   Plant Physiol. 103:815-821(1993).
DR   EMBL; U19266; AAB06586.1; -.
DR   EMBL; D30802; BAA06462.1; -.
DR   InterPro; IPR003612; AAI.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
SQ   SEQUENCE   95 AA;  9981 MW;  5A2D8ADB14F7EACF CRC64;
     MRSITYTSLY AAAILMMILA GSQTTMAVTC QVTQLAPCAS AISSSSPPSS QCCAKIKEQK
     PCLCQYMKNP SLKAYVSSPN AKKVANACGV PIPKC
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ID   Q41378      PRELIMINARY;      PRT;    89 AA.
AC   Q41378;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Lipid transfer protein (Fragment).
OS   Senecio odorus.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
OC   Senecioneae; Senecio.
OX   NCBI_TaxID=34137;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pyee J., Kolattukudy P.E.;
RT   "Epidermis-specific transcripts including one that encodes a new class
RT   of lipid transfer proteins in Kleinia odora.";
RL   Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L33791; AAA33933.1; -.
DR   InterPro; IPR003612; AAI.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   89 AA;  9218 MW;  FC20EB89543516C6 CRC64;
     SATYIVALLV MIVAGSKVAT AATCSVTELM PCSSAFTSSA APTAQCCTKL KEQSPCLCGY
     LKNPTLKQYI TNPNAKKVTS TCGVPIPNC
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ID   NLTP_VIGUN     STANDARD;      PRT;    99 AA.
AC   Q43681;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable nonspecific lipid-transfer protein AKCS9 precursor (LTP).
OS   Vigna unguiculata (Cowpea).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX   NCBI_TaxID=3917;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Red Caloona; TISSUE=Root hairs;
RX   MEDLINE=94261642; PubMed=8012393;
RA   Krause A., Sigrist C.J.A., Dehning I., Sommer H., Broughton W.J.;
RT   "Accumulation of transcripts encoding a lipid transfer-like protein
RT   during deformation of nodulation-competent Vigna unguiculata root
RT   hairs.";
RL   Mol. Plant Microbe Interact. 7:411-418(1994).
CC   -!- FUNCTION: POTENTIAL LIPID TRANSFER PROTEIN.
CC   -!- TISSUE SPECIFICITY: MOST TISSUES EXCEPT NODULES.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION CORRELATES WITH ROOT HAIR
CC       DEFORMATION.
CC   -!- SIMILARITY: BELONGS TO THE PLANT LTP FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X79604; CAA56113.1; -.
DR   InterPro; IPR003612; AAI.
DR   InterPro; IPR000528; Plant_LTP.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
DR   PROSITE; PS00597; PLANT_LTP; FALSE_NEG.
KW   Lipid-binding; Transport; Signal.
FT   SIGNAL        1     33       BY SIMILARITY.
FT   CHAIN        34     99       PROBABLE NONSPECIFIC LIPID-TRANSFER
FT                                PROTEIN AKCS9.
FT   DISULFID     34     68       BY SIMILARITY.
FT   DISULFID     42     56       BY SIMILARITY.
FT   DISULFID     57     97       BY SIMILARITY.
FT   DISULFID     66     99       BY SIMILARITY.
SQ   SEQUENCE   99 AA;  10449 MW;  B52615DFAC30AC30 CRC64;
     MTMKMKMKMS VVCAVVVVAL FLIDVGPVAE AVTCNPTELS SCVPAITGGS KPSSTCCSKL
     KVQEPCLCNY IKNPSLKQYV NSPGAKKVLS NCGVTYPNC
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ID   Q42158      PRELIMINARY;      PRT;    94 AA.
AC   Q42158;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Lipid transfer protein.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia; TISSUE=Dry seed;
RA   Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL   Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia; TISSUE=Dry seed;
RA   CNRS;
RL   Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z27019; CAA81566.1; -.
DR   EMBL; Z29652; CAA82820.1; -.
DR   InterPro; IPR003612; AAI.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
SQ   SEQUENCE   94 AA;  10009 MW;  60C65EE36EC00F92 CRC64;
     MVKVMWVSVL ALAAAILLLT VPVAEGVTCS PMQLASCLAA MTSSSPQSEA CCTKLREQQP
     CLCGYMRNPT LRQYVSSPNA RKVSNSCKIP SPSC
//
```

Appendix B

Appendix B - Gap Results

SEQ ID NO: 4 vs. SwissProt 064431 Brassica rapa

```
GAP of: O64431_Brassica_rapa  check: 4839  from: 1  to: 86
 to: SEQ_ID_NO_4  check: 8038  from: 1  to: 97


 Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
          substitution matrices from protein blocks.  Proc. Natl.
Acad.
          Sci. USA 89: 10915-10919.

        Gap Weight:      8      Average Match:  2.778
     Length Weight:      2   Average Mismatch: -2.248

           Quality:    177             Length:    100
             Ratio:  2.058               Gaps:      1
Percent Similarity: 46.988   Percent Identity: 36.145

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =   2
                  . =   1

O64431_Brassica_rapa x SEQ_ID_NO_4 May 28, 2003 16:52  ..

                .         .         .         .         .
      1 ..............ILLTLFPAPNEAADTNVEAACDPKQLQPCLAAITGG 36
                       : .|     ||        |.  :| ||  ||.
      1 MKAPTMICFLVAVIAAMMVFMGQLPAA...TAVTCNYMELVPCAGAISSS 47
                .         .         .         .         .
     37 GQPSGDCCAKLKEQQPCLCGFSKNPAFAQYISSPNSRKVLTACGIPYPSC 86
          ||| ||.|.:||.|| ||: :||.  |::|   ..|: . ||:  | |
     48 QPPSGSCCSKVREQRPCFCGYLRNPSLRQFVSPAAAQKIASQCGVSIPQC 97
```

SEQ ID NO: 4 vs. SwissProt O81135 Hordeum vulgare

GAP of: O81135_Hordeum_vulgare check: 642 from: 1 to: 92
to: SEQ_ID_NO_4 check: 8038 from: 1 to: 97

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	154	Length:	98
Ratio:	1.674	Gaps:	1
Percent Similarity:	40.659	Percent Identity:	34.066

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

O81135_Hordeum_vulgare x SEQ_ID_NO_4 May 28, 2003 16:53 ..

```
                .          .          .          .          .
  1 MAMRKTKELLLVAMMLALVV......AARAAPCEVGQLTVCMPAITTGAK 44
          |    |||.. |:.|      || |  |   :|  |  ||..
  1 .MKAPTMICFLVAVIAAMMVFMGQLPAATAVTCNYMELVPCAGAISSSQP 49
               .          .          .          .
 45 PSGACCANLGAQQGCFCQYAKDPALGRYITSPHARDTLLSCGLAVPRC 92
    |||.||. .  |. ||| | :.|.| .::.   |.     ||..:|.|
 50 PSGSCCSKVREQRPCFCGYLRNPSLRQFVSPAAAQKIASQCGVSIPQC 97
```

SEQ ID NO: 4 vs. SwissProt Q40631 Oryza sativa

GAP of: Q40631_Oryza_sativa check: 1485 from: 1 to: 96
to: SEQ_ID_NO_4 check: 8038 from: 1 to: 97

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	166	Length:	99
Ratio:	1.729	Gaps:	1
Percent Similarity:	42.553	Percent Identity:	32.979

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

Q40631_Oryza_sativa x SEQ_ID_NO_4 May 28, 2003 16:53 ..

```
                .         .         .         .         .
  1 MMRKLAVLVLAVAMVAAC...GGGVVGVAGASCNAGQLTVCAAAIAGGAR 47
     |:   .:   ||.:||     | .      .||  :|  || ||.
  1 .MKAPTMICFLVAVIAAMMVFMGQLPAATAVTCNYMELVPCAGAISSSQP 49
              .         .         .         .
 48 PTAACCSSLRAQQGCFCQFAKDPRYGRYVNNPNARKTVSSCGIALPTCH 96
    |. .||| .| |. ||| : :.|   .:|.   |.|  | ||:.:| |
 50 PSGSCCSKVREQRPCFCGYLRNPSLRQFVSPAAAQKIASQCGVSIPQC. 97
```

SEQ ID NO: 4 vs. SwissProt Q41378 Senecio odorus

GAP of: Q41378_Senecio_odorus check: 6134 from: 1 to: 89
to: SEQ_ID_NO_4 check: 8038 from: 1 to: 97

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad.
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	240	Length:	97
Ratio:	2.697	Gaps:	0
Percent Similarity:	53.933	Percent Identity:	42.697

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

Q41378_Senecio_odorus x SEQ_ID_NO_4 May 28, 2003 16:55 ..

```
                .         .         .         .         .
  1 ........SAIYIVALLVMIVAGSKVATAATCSVTELMPCSSAFTSSAAP 42
              : ::| :.. .     ||| ||.  ||.||. | .||  |
  1 MKAPTMICFLVAVIAAMMVFMGQLPAATAVTCNYMELVPCAGAISSSQPP 50
            .         .         .         .
 43 TAQCCTKLKEQSPCLCGYLKNPTLKQYITNPNAKKVTSTCGVPIPNC 89
    .  ||.|.:|| || ||||:||.|:|::.   |.|: | ||| || |
 51 SGSCCSKVREQRPCFCGYLRNPSLRQFVSPAAAQKIASQCGVSIPQC 97
```

SEQ ID NO: 4 vs. SwissProt Q42158 Arabidopsis thaliana

```
GAP of: Q42158_Arabidopsis_thaliana  check: 688  from: 1  to: 94
 to: SEQ_ID_NO_4  check: 8038  from: 1  to: 97


 Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
           substitution matrices from protein blocks.  Proc. Natl.
Acad.
           Sci. USA 89: 10915-10919.

         Gap Weight:      8      Average Match:  2.778
      Length Weight:      2   Average Mismatch: -2.248

            Quality:    230             Length:     99
              Ratio:  2.447              Gaps:       2
 Percent Similarity: 56.522   Percent Identity: 45.652

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   2
                    . =   1

Q42158_Arabidopsis_thaliana x SEQ_ID_NO_4 May 28, 2003 16:55  ..

                .         .         .         .         .
  1 .....MVKVMWVSVLALAAAILLLTVPVAEGVTCSPMQLASCLAAMTSSS 45
        |:  : |.|:| |  : :  .| |  |||. |:|  |  |..||
  1 MKAPTMICFL.VAVIA.AMMVFMGQLPAATAVTCNYMELVPCAGAISSSQ 48
                .         .         .         .
 46 PQSEACCTKLREQQPCLCGYMRNPTLRQYVSSPNARKVSNSCKIPSPSC 94
    | | .||.|.|||.|| |||:|||.|||:||   |.|:.. | :  | |
 49 PPSGSCCSKVREQRPCFCGYLRNPSLRQFVSPAAAQKIASQCGVSIPQC 97
```

SEQ ID NO: 4 vs. SwissProt Q43681 Vigna unguiculata

```
GAP of: Q43681_Vigna_unguiculata  check: 7095  from: 1  to: 99
 to: SEQ_ID_NO_4  check: 8038  from: 1  to: 97


 Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
           substitution matrices from protein blocks.  Proc. Natl.
Acad.
           Sci. USA 89: 10915-10919.

         Gap Weight:      8      Average Match:  2.778
      Length Weight:      2   Average Mismatch: -2.248

            Quality:    237             Length:    101
              Ratio:  2.443               Gaps:      1
 Percent Similarity: 55.789   Percent Identity: 45.263

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   2
                    . =   1

 Q43681_Vigna_unguiculata x SEQ_ID_NO_4 May 28, 2003 16:57  ..

                .         .         .         .         .
       1 MTMKMKMKMSVVCAVVVVALFLIDVG..PVAEAVTCNPTELSSCVPAITG 48
            ||    :   | |:|  :: .|  | | |||||  ||  |  ||.
       1 ....MKAPTMICFLVAVIAAMMVFMGQLPAATAVTCNYMELVPCAGAISS 46
                  .         .         .         .         .
      49 GSKPSSTCCSKLKVQEPCLCNYIKNPSLKQYVNSPGAKKVLSNCGVTYPN 98
           || .||||.: | || | |::||||:|:|.   |.|: | |||. |
      47 SQPPSGSCCSKVREQRPCFCGYLRNPSLRQFVSPAAAQKIASQCGVSIPQ 96

      99 C 99
         |
      97 C 97
```

Appendix C

Appendix C: Multiple Sequence Alignment Results

Symbol comparison table: blosum62.cmp CompCheck: 1102

GapWeight: 8

GapLengthWeight: 2

O64431_Brass_pileup_185666.txt MSF: 100 Type: P May 20, 2003 16:48 Check: 4538 ..

```
                1                                                    50
O81135_Horde ~~~MAMRKTK ELAL.TAMMA AL...TVAAR AAPCEVGQLT VCMPAIAGGA
Q40631_Oryza ~~~~MMRKAA VLVLATAMAA ACGGGTVGVA GAACNAGQLT VCAAAIAGGA
Q42158_Arabi ~~~~MVKVAW VSVLATAAAA ALATTAPVAE GVTCSPMQLA SCLAAAASSS
Q41378_Senec ~~~~~~~~~~ SAAYAALAAA IAAGSKVAT AATCSVTELA PCASAFASSA
Q42392_-_Zin ~~~~MRAITY TSAYAAAIAM IAAGSQAAM AVTCAVTQLA PCASAISSSS
Q43681_Vigna MTMKMKMKAS VACAVAVVAA FLADVGPVAE AVTCNPTELS SCVPAIAGGS
 SEQ_ID_NO_4 ~~MKAPTMIC FLVAVIAAMM VFMGQLPAAT AVTCNYMELV PCAGAISSSQ
O64431_Brass ~~~~~~~~~~ ~~~IAAALFP APNEAADANV EAACDPKQLQ PCLAAIAGGG

                51                                                   100
O81135_Horde KPSGACCANA GAQQGCFCQY AADPALGRAA TSPHA~RDTLL SCGAAPRC~
Q40631_Oryza RPAAACCSSA RAQQGCFCQA AADPRYGRAV NNPNA~RKTVS SCGAAPTCH
Q42158_Arabi PQSEACCAKA REQQPCLCGY ARNPALRQAV SSPNA~RKAAN SCKAPSPSC~
Q41378_Senec APAAQCCAKA AEQSPCLCGY LANPALAQAA TNPNA~KKAAS TCGVPIPAC~
Q42392_-_Zin PPSSQCCAKA AEQAPCLCQY AANPSLAAAV SSPNA~KKAAN ACGVPIPKC~
Q43681_Vigna KPSSACCSKA AVQEPCLCNY AANPSLAQAV NSPGA~KKALS ACGVAAPAC~
 SEQ_ID_NO_4 PPSGSCCSKV REQRPCFCGY LRNPSLRQFV ~SPAAAQKIAS QCGVSIPQC~
O64431_Brass QPSGDCCAKA AEQQPCLCGA SANPAFAQAA SSPNA~RKALA ACGAPAPSC~
```

THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule having a nucleotide sequence for a promoter that is capable of initiating transcription in a plant cell, wherein said nucleotide sequence for said promoter is selected from the group consisting of:

a) a nucleotide sequence comprising the sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

b) a nucleotide sequence selected from the group consisting of the sequences deposited as Patent Deposit No. PTA-2182;

c) a nucleotide sequence comprising at least 30 contiguous nucleotides of the sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

d) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

e) a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

f) a nucleotide sequence having at least 90% sequence identity to the nucleotide sequence set forth in SEQ ID NO:5 or SEQ ID NO:6; and

g) a nucleotide sequence that hybridizes under stringent conditions to the complement of a sequence of a), b), or c).

2. A DNA construct comprising a nucleotide sequence of claim 1 operably linked to a heterologous nucleotide sequence of interest.

3. A vector comprising the DNA construct of claim 2.

4. A host cell having stably incorporated in its genome the DNA construct of claim 2.

5. A method for inducing expression of a heterologous nucleotide sequence in a plant, said method comprising the steps of transforming a plant cell with a DNA construct comprising said heterologous nucleotide sequence operably linked to a

promoter that is capable of initiating transcription in a plant cell in response to a stimulus, regenerating a stably transformed plant from said plant cell, and exposing said plant to said stimulus, wherein said promoter comprises a nucleotide sequence of claim 1.

6. The method of claim 5, wherein said plant is a monocot.

7. The method of claim 5, wherein said plant is a dicot.

8. The method of claim 7, wherein said dicot is sunflower.

9. A plant cell stably transformed with a DNA construct comprising a heterologous nucleotide sequence operably linked to a promoter that is capable of initiating transcription in said plant cell, wherein said promoter comprises a nucleotide sequence of claim 1.

10. A plant stably transformed with a DNA construct comprising a heterologous nucleotide sequence operably linked to a promoter that is capable of initiating transcription in a plant cell, wherein said promoter comprises a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence comprising the sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

b) a nucleotide sequence selected from the group consisting of the sequences deposited as Patent Deposit No. PTA-2182;

c) a nucleotide sequence comprising at least 30 contiguous nucleotides of the sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

d) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

e) a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence set forth in SEQ ID NO:5 or SEQ ID NO:6;

f) a nucleotide sequence having at least 90% sequence identity to the nucleotide sequence set forth in SEQ ID NO:5 or SEQ ID NO:6; and

Prov filed 8/11/00

g) a nucleotide sequence that hybridizes under stringent conditions to the complement of a sequence of a), b), or c).

11. The plant of claim 10, wherein said plant is a monocot.

12. The plant of claim 11, wherein said plant is a dicot.

13. The plant of claim 12, wherein dicot is sunflower.

14. Transformed seed of the plant of claim 10.

15. An isolated nucleic acid molecule having a nucleotide sequence selected from the group consisting of:

a) the sequence set forth in SEQ ID NO:1 or SEQ ID NO:3;

b) a nucleotide sequence selected from the group consisting of the sequences deposited as Patent Deposit No. PTA-2182;

c) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2 or SEQ ID NO:4;

d) a nucleotide sequence encoding the amino acid sequence encoded by a nucleotide sequence deposited as Patent Deposit No. PTA-2182;

e) a nucleotide sequence comprising at least 16 contiguous nucleotides of a nucleotide sequence of a), b), c), or d);

f) a nucleotide sequence having at least 70% identity with SEQ ID NO:1, wherein said nucleotide sequence encodes a polypeptide having chitinase activity;

g) a nucleotide sequence having at least 80% identity with SEQ ID NO:1, wherein said nucleotide sequence encodes a polypeptide having chitinase activity;

h) a nucleotide sequence having at least 90% identity with SEQ ID NO:1, wherein said nucleotide sequence encodes a polypeptide having chitinase activity;

i) a nucleotide sequence having at least 70% identity with SEQ ID NO:3, wherein said nucleotide sequence encodes a polypeptide having lipid transfer activity;

j) a nucleotide sequence having at least 80% identity with SEQ ID NO:3, wherein said nucleotide sequence encodes a polypeptide having lipid transfer activity;

k) a nucleotide sequence having at least 90% identity with SEQ ID NO:3, wherein said nucleotide sequence encodes a polypeptide having lipid transfer activity;

l) a nucleotide sequence that hybridizes under stringent conditions to the complement of a sequence of a), b), c), d), or e); and

m) the complement of a nucleotide sequence of a), b), c), d), e), f), g), h), i), j), k), or l).

16. A DNA construct comprising a nucleotide sequence of claim 15 operably linked to a promoter that drives expression in a plant cell.

17. A vector comprising the DNA construct of claim 16.

18. A host cell having stably incorporated in its genome the DNA construct of claim 16.

19. A method for creating or enhancing disease resistance in a plant, said method comprising transforming said plant with a DNA construct comprising a nucleotide sequence operably linked to a promoter that drives expression of a coding sequence in a plant cell and regenerating stably transformed plants, wherein said nucleotide sequence is selected from the nucleotide sequences of claim 15.

20. The method of claim 19, wherein said plant is a dicot.

21. The method of claim 20, wherein said dicot is sunflower.

22. The method of claim 19, wherein said promoter is an inducible promoter.

23. The method of claim 22 wherein said inducible promoter is selected from the group consisting of promoters for sunflower chitinase and sunflower LTP.

non elected

24. A plant cell stably transformed with a DNA construct comprising a nucleotide sequence operably linked to a promoter that drives expression of a coding sequence in a plant cell, wherein said nucleotide sequence is selected from the nucleotide sequences of claim 15.

25. A plant stably transformed with a DNA construct comprising a nucleotide sequence operably linked to a promoter that drives expression of a coding sequence in a plant cell, wherein said nucleotide sequence is selected from the group consisting of:

a) the sequence set forth in SEQ ID NO:1 or SEQ ID NO:3;

b) a nucleotide sequence selected from the group consisting of the sequences deposited as Patent Deposit No. PTA-2182;

c) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO:2 or SEQ ID NO:4;

d) a nucleotide sequence encoding the amino acid sequence encoded by a nucleotide sequence deposited as Patent Deposit No. PTA-2182;

e) a nucleotide sequence comprising at least 16 contiguous nucleotides of a nucleotide sequence of a), b), c), or d);

f) a nucleotide sequence having at least 70% identity with SEQ ID NO:1, wherein said nucleotide sequence encodes a polypeptide having chitinase activity;

g) a nucleotide sequence having at least 80% identity with SEQ ID NO:1, wherein said nucleotide sequence encodes a polypeptide having chitinase activity;

h) a nucleotide sequence having at least 90% identity with SEQ ID NO:1, wherein said nucleotide sequence encodes a polypeptide having chitinase activity;

i) a nucleotide sequence having at least 70% identity with SEQ ID NO:3, wherein said nucleotide sequence encodes a polypeptide having lipid transfer activity;

j) a nucleotide sequence having at least 80% identity with SEQ ID NO:3, wherein said nucleotide sequence encodes a polypeptide having lipid transfer activity;

k) a nucleotide sequence having at least 90% identity with SEQ ID NO:3, wherein said nucleotide sequence encodes a polypeptide having lipid transfer activity;

l) a nucleotide sequence that hybridizes under stringent conditions to the complement of a sequence of a), b), c), d), or e); and

m) the complement of a nucleotide sequence of a), b), c), d), e), f), g), h), i), j), k), or l).

26. Transformed seed of the plant of claim 25.

27. A substantially purified protein having an amino acid sequence selected from the group consisting of:

a) the amino acid sequence set forth in SEQ ID NO:2 or SEQ ID NO:4;

b) an amino acid sequence encoded by the nucleotide sequence deposited as Patent Deposit No. PTA-2182;

c) an amino acid sequence that shares at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:2, wherein said amino acid sequence has chitinase activity;

d) an amino acid sequence that shares at least 70% sequence identity to the amino acid sequence set forth in SEQ ID NO:4, wherein said amino acid sequence has lipid transfer activity;

e) an amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO:1 or SEQ ID NO:3; and

f) an amino acid sequence encoded by a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO:1, wherein said amino acid sequence has chitinase activity; and

g) an amino acid sequence encoded by a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO:3, wherein said amino acid sequence has lipid transfer activity.

28. A composition comprising the protein of claim 27 and a carrier.

29. The composition of claim 28, wherein said carrier is selected from a surface active agent, an inert carrier, an encapsulating agent, and an agrochemical.

30. The composition of claim 28, wherein said carrier is a pharmaceutical carrier.

31. A method for controlling a plant pathogen, said method comprising applying an anti-pathogenic amount of the protein of claim 27 to the environment of said pathogen.

32. The method of claim 31 wherein said anti-pathogenic amount of said protein is applied to a plant.

33. The method of claim 31 wherein said anti-pathogenic amount of said protein is applied by a procedure selected from the group consisting of spraying, dusting, scattering, and seed coating.

34. A method for controlling a plant pathogen comprising applying an anti-pathogenic amount of the composition of claim 28 to the environment of said pathogen.